

SEQUENCE LISTING

<110> Hoxie, James A.
Lin, George

<120> Compositions, Methods and Kits Relating to Deletion Mutations of
Immunodeficiency Virus gp120 Hypervariable Regions

<130> 053893-5046

<150> 60/443,364

<151> 2003-01-29

<160> 30

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> HIV-2/VCP (env)

<400> 1

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 <213> HIV-2/VCP (gp120)
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 <212> DNA
 <213> HIV-2/VCP (gp41)

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 <212> PRT
 <213> HIV-2/VCP (env)

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 35 40 45
 Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr

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Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr 85 90 95		
Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn 100 105 110		
Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn 115 120 125		
Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys 130 135 140		
Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr 145 150 155 160		
Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Glu Ala Trp Tyr Ser 165 170 175		
Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr 180 185 190		
Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His 195 200 205		
Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala 210 215 220		
Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys 225 230 235 240		
Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser 245 250 255		
Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr 260 265 270		
Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn 275 280 285		

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val
290 295 300

Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn
305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
325 330 335

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
340 345 350

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
355 360 365

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
370 375 380

Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg
385 390 395 400

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
405 410 415

Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg
420 425 430

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
435 440 445

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
450 455 460

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
465 470 475 480

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
485 490 495

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu
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Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Leu Thr Leu Thr Ala
515 520 525

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu
530 535 540

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp
545 550 555 560

Gly Thr Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu
565 570 575

Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val
580 585 590

Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp
595 600 605

Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu
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Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys
625 630 635 640

Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn
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Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr
660 665 670

Val Val Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln
675 680 685

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro
690 695 700

Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro
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Ser Trp Leu

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<212> PRT
<213> HIV-2/VCP (gp120)

<400> 5

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35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Glu Ala Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
 195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
 210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
 225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
 245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
 260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
 275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Thr Val
 290 295 300

Leu Pro Ile Met Ser Gly Phe Lys Phe His Ser Lys Pro Val Ile Asn
 305 310 315 320

Lys Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
 325 330 335

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
 340 345 350

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
 355 360 365

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
 370 375 380

Phe Leu Tyr Cys Asn Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg
 385 390 395 400

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
 405 410 415

Ile Asn Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg
420 425 430

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
435 440 445

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
450 455 460

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
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Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
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Gln Arg His Thr Arg
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<212> PRT
<213> HIV-2/VCP (gp41)

<400> 6

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35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp

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Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr 145 150 155 160		
Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile 165 170 175		
Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu 180 185 190		
Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln 195 200 205		
Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr 210 215 220		
Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile 225 230 235 240		
Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly 245 250 255		
Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu 260 265 270		
Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp 275 280 285		
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gagactcttg caggcgcggg g	2181

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 <211> 1209
 <212> DNA
 <213> HIV-2/VCP Clone p16.5 (gp120)

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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ctgtacagtg cttgccagac	180
aatgatgatt atcaggaaat agctttaaat gtaacagagg ctttcgatgc atgggataat	240
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catacaaga	1209

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 <211> 972
 <212> DNA
 <213> HIV-2/VCP Clone p16.5 (gp41)

<400> 9	
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gcgtcgggtga cgctgaccgc tcagtcccgg acttcattga ctgggatagt gcagcaacag	120
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga	180
actaaaaatc tccaggcaag agtcactgct atagagaaat acctaaagga ccaggcgcag	240
ctaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaa	300
gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca aaaagtccgc	360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat	420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc	480
tcctgggtca ggtatattca atatggagtt tacgtagtag taggaatagt agctttaaga	540
atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc	600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc	660
agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gctttagccg	720
atagcatata ttcatttcct gatccgcctg ctgattcgcc tcttgatcgg gctatacaac	780
atctgcagag acttactatc caggatctcc ccgatcctcc aaccaatctt ccagagtctc	840
cagagagcac taacagcaat cagagactgg ctgaggctta aagcagccta cctgcagtat	900
gggtgcgagt ggatccaaga agcgttccaa gcccttgcaa ggactacaag agagactctt	960
gcaggcgcgg gg	972

<210> 10
 <211> 726
 <212> PRT
 <213> HIV-2/VCP Clone p16.5 (env)

<400> 10

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
 100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp
 115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
 130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
 145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
 165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr
 180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly
290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr
405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser

420	425	430
Arg Thr Ser Leu Thr Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp		
435	440	445
Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr		
450	455	460
Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp		
465	470	475
480		
Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His		
485	490	495
Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn		
500	505	510
Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn		
515	520	525
Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu		
530	535	540
Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu		
545	550	555
560		
Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val		
565	570	575
Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu		
580	585	590
Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly		
595	600	605
Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg		
610	615	620
Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp		
625	630	635
640		
Leu Pro Ile Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu		
645	650	655

Leu Ile Gly Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser
660 665 670

Pro Ile Leu Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala
675 680 685

Ile Arg Asp Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys
690 695 700

Glu Trp Ile Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu
705 710 715 720

Thr Leu Ala Gly Ala Gly
725

<210> 11
<211> 403
<212> PRT
<213> HIV-2/VCP Clone p16.5 (gp120)

<400> 11

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Lys Glu Ser Cys Asp Lys His Tyr Trp
 115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
 130 135 140

Arg Cys Asn Asp Ile Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
 145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
 165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Thr Glu Asn Arg Thr Tyr Ile Tyr
 180 185 190

Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
 195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
 210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
 225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
 245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
 260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
 275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Asp Asn Arg Thr Gly
 290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
 305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
 325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp

340

345

350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
 355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
 370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
 385 390 395 400

His Thr Arg

<210> 12

<211> 323

<212> PRT

<213> HIV-2/VCP Clone p16.5 (gp41)

<400> 12

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
 1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
 20 25 30

Leu Thr Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
 50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
 85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
 100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
 115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu Pro Ile
225 230 235 240

Ala Tyr Ile His Phe Leu Ile Arg Leu Leu Ile Arg Leu Leu Ile Gly
245 250 255

Leu Tyr Asn Ile Cys Arg Asp Leu Leu Ser Arg Ile Ser Pro Ile Leu
260 265 270

Gln Pro Ile Phe Gln Ser Leu Gln Arg Ala Leu Thr Ala Ile Arg Asp
275 280 285

Trp Leu Arg Leu Lys Ala Ala Tyr Leu Gln Tyr Gly Cys Glu Trp Ile
290 295 300

Gln Glu Ala Phe Gln Ala Leu Ala Arg Thr Thr Arg Glu Thr Leu Ala
305 310 315 320

Gly Ala Gly

<210> 13
<211> 1926
<212> DNA
<213> HIV-2/VCP Clone p16.7 (env)

<400> 13

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cattgcaagc aatttgtgac tgttttctat ggcataccg cgtggaggaa tgcattccatt	120
cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac	180
aatgatgatt atcaggaaat agctttaaat gtaacagagg ctttcgatgc atgggataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ctgagacatc aataaaacca	300
tgtgtcaaat taacaccctt atgtgtaggt gccggccatt gcaatacatc agtcatcaca	360
gagtcagtgtg ataagcacta ttgggatgct atgaggttta gatactgtgc accaccgggt	420
tttgccttac taagatgcaa tgataactaat tattcaggct ttgcacctaa ttgctctaaa	480
gtagtagctg ctacatgcac cagaatgatg gaaacgcaat cttctacatg gtttggcttt	540
aatggcacta gagcagaaaa tagaacatat atctattggc atggtaaaaa tgacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
ggtgccggca aaccaggca agcatggtgt tggttcaaag gcgaatggaa ggaagccatg	720
caggagggtga aggagaccct tgcgaaacat cctagatata aagggaacag gagccgcaca	780
gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg	840
actaactgca gaggggaatt tctctactgc gacatgactt ggttcctcaa ttgggtagaa	900
aacaggacgg gtcagaaaca gcgtaattat gcaccgtgcc atataaggca aataattaat	960
acttggcaca gggtagggaa aaacgtatat ttgcctccca gggaaagggga gttaacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgcag aggtggcaga actataaccgg ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200
catacaagag gtgtgttcgt gctagggttc ttgggttttc tcgcaacggc aggttctgca	1260
atgggcgcgg cgtcggtgac gctgaccgct cagtcccga cttcattgac tggggtagtg	1320
cagcaacagc aacagctgtt ggatgtggtc aagaaacaac aagaaatgtt gcgactgacc	1380
gtctggggaa ctaaaaatct ccaggcaaga gtcactgcta tagagaaata cctaaaggac	1440
caggcgcagc taaattcatg gggatgtgcg tttagacaag tctgccacac ttctgtacca	1500
tgggtaaatg atagcttgac acctgattgg aacaatatga cgtggcagga atgggaacaa	1560
aaagtccgct actgggaggc aaatatcagt caaagtctag aacaagcaca aattcagcaa	1620
gaaaagaatt tgtatgagct gcaaaaatta aatagctggg gtgtttttac caattggctt	1680

gacttcacct cctgggtcag gtatatccaa tatggagttt atgtagtagt aggaatagta	1740
gctttaagaa tagtaatata tatagtacag atgttgagta gacttaggaa gggctatagg	1800
cctgttttct cctccccccc cggttatatc caacagatcc atatccacaa ggaccaggaa	1860
cagccagcca gagaagaaac agaagaagac gttggaagca acggtggaga caaatcttgg	1920
cttttag	1926

<210> 14
 <211> 1209
 <212> DNA
 <213> HIV-2/VCP Clone p16.7 (gp120)

<400> 14	
atgaagggtgta gtaagaatca accgctgatt gctattgtac tagctagtgc ttacctaaca	60
cattgcaagc aatttgtgac tgttttctat ggcatacccg cgtggaggaa tgcattccatt	120
cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccgtacagtg cttgccagac	180
aatgatgatt atcaggaaat agctttaaat gtaacagagg ctttcgatgc atgggataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ctgagacatc aataaaacca	300
tgtgtcaaata taacaccctt atgtgtaggt gccggccatt gcaatacatc agtcatacaca	360
gagtcagtgtg ataagcacta ttgggatgct atgaggttta gatactgtgc accaccgggt	420
tttgccttac taagatgcaa tgataactaat tattcaggct ttgcacctaa ttgctctaaa	480
gtagtagctg ctacatgcac cagaatgatg gaaacgcaat cttctacatg gtttggcttt	540
aatggcacta gagcagaaaa tagaacatat atctattggc atggtaaaaa tgacagaact	600
attatcagct taaataactt ttataatctc actatgcatt gtaagaggcc gggaaataag	660
gggtgccggca aaccaggca agcatggtgt tggttcaaag gcgaatggaa ggaagccatg	720
caggaggtga aggagaccct tgcgaaacat cctagatata aagggaacag gagccgcaca	780
gagaatatta aatttaaagc accaggaaga ggctcagacc cagaagcagc atacatgtgg	840
actaactgca gaggggaatt tctctactgc gacatgactt ggttcctcaa ttgggtagaa	900
aacaggacgg gtcagaaaca gcgtaattat gcaccgtgcc atataaggca aataattaat	960
acttggcaca gggtagggaa aaacgtatat ttgcctcca gggaagggga gttaacctgc	1020
aactcaacag tgaccagcat aattgccaac attgatacgg gagatcaaac agatattacc	1080
tttagtgcag aggtggcaga actataccgg ttggaattgg gagattacaa attagtagaa	1140
atcacaccaa ttggcttcgc acctacatca gtaaagagat actcctctgc tcaccagaga	1200

catacaaga

1209

<210> 15
<211> 717
<212> DNA
<213> HIV-2/VCP Clone p16.7 (gp41)

<400> 15
gggtgtgttcg tgctaggggtt cttggggtttt ctcgcaacgg caggttctgc aatggg'gcgcg 60
gcgtcgggtga cgctgaccgc tcagtcccgg acttcattga ctggggtagt gcagcaacag 120
caacagctgt tggatgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180
actaaaaatc tccaggcaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240
ctaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaat 300
gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca aaaagtccgc 360
tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480
tcctgggtca ggtatattca atatggagtt tatgtagtag taggaatagt agctttaaga 540
atagtaatat atatagtaca gatgttgagt agacttagga agggctatag gcctgttttc 600
tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
agagaagaaa cagaagaaga cgttggaagc aacggtggag acaaactctg gctttag 717

<210> 16
<211> 641
<212> PRT
<213> HIV-2/VCP Clone p16.7 (env)

<400> 16

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser
1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly
 290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
 305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
 325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
 340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
 355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
 370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
 385 390 395 400

His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr
 405 410 415

Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser
 420 425 430

Arg Thr Ser Leu Thr Gly Val Val Gln Gln Gln Gln Gln Leu Leu Asp
 435 440 445

Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr
 450 455 460

Lys Asn Leu Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp
 465 470 475 480

Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His
 485 490 495

Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn
 500 505 510

Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn

515

520

525

Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu
 530 535 540

Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu
 545 550 555 560

Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val
 565 570 575

Val Gly Ile Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu
 580 585 590

Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly
 595 600 605

Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg
 610 615 620

Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp
 625 630 635 640

Leu

<210> 17
 <211> 403
 <212> PRT
 <213> HIV-2/VCP Clone p16.7 (gp120)

<400> 17

Met Lys Gly Ser Lys Asn Gln Pro Leu Ile Ala Ile Val Leu Ala Ser
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Val Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asp Asn
65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Ser Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly Ala Gly
100 105 110

His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His Tyr Trp
115 120 125

Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala Leu Leu
130 135 140

Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys Ser Lys
145 150 155 160

Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser Ser Thr
165 170 175

Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile Tyr
180 185 190

Trp His Gly Lys Asn Asp Arg Thr Ile Ile Ser Leu Asn Asn Phe Tyr
195 200 205

Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala Gly Lys
210 215 220

Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu Ala Met
225 230 235 240

Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys Gly Asn
245 250 255

Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg Gly Ser
260 265 270

Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu Phe Leu
275 280 285

Tyr Cys Asp Met Thr Trp Phe Leu Asn Trp Val Glu Asn Arg Thr Gly
 290 295 300

Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile Ile Asn
 305 310 315 320

Thr Trp His Arg Val Gly Lys Asn Val Tyr Leu Pro Pro Arg Glu Gly
 325 330 335

Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn Ile Asp
 340 345 350

Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala Glu Leu
 355 360 365

Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr Pro Ile
 370 375 380

Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His Gln Arg
 385 390 395 400

His Thr Arg

<210> 18
 <211> 238
 <212> PRT
 <213> HIV-2/VCP Clone p16.7 (gp41)

<400> 18

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
 1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
 20 25 30

Leu Thr Gly Val Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
 50 55 60

Gln Ala Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
165 170 175

Val Ala Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Lys Ser Trp Leu
225 230 235

<210> 19
<211> 2427
<212> DNA
<213> HIV-2/VCP Clone p16.9 (env)

<400> 19
atgaagggtgta gtaagaatca actgctgatt gctattatac tagctagtgc ttacctaaca 60
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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300

tgtgtcaa	at	taacaccctt	atgtgtagca	atgaactgta	caaggaacat	gaccacatcc	360
acagggacca	cagacaccca	aaatatcaca	attataaatg	acacttcgcc	atgcgtacgt		420
gcagacaact	gcacaggatt	aaaggaggaa	gaaatggtcg	actgtcagtt	taatatgaca		480
ggattagaga	gagacaagag	aaaacagtat	actggagcat	ggtactcaaa	agatgtgatt		540
tgtgacaata	acacctcaag	tcggagcaag	tgttacatga	accattgcaa	tacatcagtc		600
atcacagagt	catgtgataa	gcactattgg	gatgctatga	ggttttagata	ctgtgcacca		660
ccgggttttg	ccctactaag	atgcaatgat	actaattatt	caggctttgc	acctaattgc		720
tctaaagtag	tagctgctac	atgcaccaga	atgatggaaa	cgcaatcttc	tacatgggttt		780
ggatttaatg	gcactagagc	agaaaaataga	acatatatct	attggcatgg	taaaaataac		840
agaactatta	tcagcttaaa	taacttttat	aatctcacta	tgcattgtaa	gaggccggga		900
aataagggtg	ccggcaaacc	caggcaagca	tggtgttgg	tcaaaggcga	atggaaggaa		960
gcatgcagg	aggtgaagga	gacccttgcg	aaacatccca	gatataaagg	gaacaggagc		1020
cgcacagaga	atattaaatt	taaagcacca	ggaagaggct	cagacccaga	agcagcatat		1080
atgtggacta	actgcagagg	ggaatttctc	tactgcaaca	tggtttggtt	cctcaattgg		1140
gtagataaca	ggacgggtca	gaaacagcgc	aattatgcac	cgtgccatat	aaggcaaata		1200
attaatactt	ggcacagggt	agggaaaaac	atatatttgc	ctcccaggga	aggggagttg		1260
acctgcaact	caacagtgac	cagcataatt	gccaacattg	atacgggaga	tcaaacagat		1320
attaccttta	gtgcagaggt	ggcagaacta	taccgattgg	aattgggaga	ttacaaatta		1380
gtagaaatca	caccaattgg	cttcgcacct	acatcagtaa	agagatactc	ctctgctcac		1440
cagagacata	caagagggtg	gttcgtgcta	gggttcttgg	gttttctcgc	aacggcaggt		1500
tctgcaatgg	gcgcggcgct	ggtgacgctg	accgcccagt	cccggacttc	attggctggg		1560
atagtgcagc	aacagcaaca	gctgttggac	gtggtcaaga	aacaacaaga	aatgttgcca		1620
ctgaccgtct	ggggaactaa	aaatctccag	acaagagtca	ctgctataga	gaaataccta		1680
aaggaccagg	cgcagttaaa	ttcatgggga	tgtgcgttta	gacaagtctg	ccacacttct		1740
gtaccatggg	taaatgatag	cttgacacct	gattggaaca	atatgacgtg	gcaggaatgg		1800
gaacagaaaag	tccgctactg	ggaggcaaat	atcagtcaaa	gtctagaaca	agcacaaatt		1860
cagcaagaaa	agaatttgta	tgagctgcaa	aaattaaata	gctgggggtg	ttttaccaat		1920
tggttgact	tcacctctg	ggtcagggtat	attcaatatg	gagtttatgt	agtagtagga		1980

atagtaactt taagaatagt aatatatata gtacagatgt taagtagact taggaagggc	2040
tataggcctg ttttctcctc ccccccggt tatatccaac agatccatat ccacaaggac	2100
caggaacagc cagccagaga agaaacagaa gaagacgttg gaagcaacgg tggagacaga	2160
tcttggcttt agccgatagc atatattcat ttcctgatcc gcctgctgat tcgcctcttg	2220
atcgggctat acaacatctg cagagactta ctatccagga tctccccgat cctccaacca	2280
atcttccaga gtctccagag agcactaaca gcaatcagag actggctgag gcttaaagca	2340
gcctacctgc agtatgggtg cgagtggatc caagaagcgt tccaagccct tgcaaggact	2400
acaagagaga ctcttgacagg cgcgggg	2427

<210> 20
 <211> 1455
 <212> DNA
 <213> HIV-2/VCP Clone p16.9 (gp120)

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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac	180
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat	240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca	300
tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc	360
acagggacca cagacacca aaatatcaca attataaatg acacttcgcc atgcgtacgt	420
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggattagaga gagacaagag aaaacagtat actggagcat ggtactcaa agatgtgatt	540
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacagagt catgtgataa gcactattgg gatgctatga ggtttagata ctgtgcacca	660
ccgggttttg ccctactaag atgcaatgat actaattatt caggctttgc acctaatgc	720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt	780
ggatttaatg gcactagagc agaaaataga acatatatct attggcatgg taaaaataac	840
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gaggccggga	900
aataaggggtg ccggcaaacc caggcaagca tgggtgttgg tcaaaggcga atggaaggaa	960
gcatgcagg aggtgaagga gacccttgcg aaacatccca gatataaagg gaacaggagc	1020

cgcacagaga atattaaatt taaagcacca ggaagaggct cagacccaga agcagcatac 1080
 atgtgggacta actgcagagg ggaattttctc tactgcaaca tggcttggtt cctcaattgg 1140
 gtagataaca ggacgggtca gaaacagcgc aattatgcac cgtgccatat aaggcaaata 1200
 attaatactt ggcacaggggt agggaaaaaac atatatttgc ctcccaggga aggggagttg 1260
 acctgcaact caacagtgac cagcataatt gccaacattg atacgggaga tcaaacagat 1320
 attaccttta gtgcagagggt ggcagaacta taccgattgg aattgggaga ttacaaatta 1380
 gtagaaatca caccaattgg ctctgcacct acatcagtaa agagatactc ctctgctcac 1440
 cagagacata caaga 1455

<210> 21
 <211> 717
 <212> DNA
 <213> HIV-2/VCP Clone p16.9 (gp41)

<400> 21
 ggtgtgttcg tgctaggggt cttgggtttt ctgcgaacgg caggttctgc aatgggagcg 60
 gcgtcgggtga cgctgaccgc ccagtcccggt acttcattgg ctgggatagt gcagcaacag 120
 caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180
 actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240
 ttaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaata 300
 gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca gaaagtccgc 360
 tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
 ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480
 tcctgggtca ggtatattca atatggagtt tatgtagtag taggaatagt aactttaaga 540
 atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc 600
 tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
 agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gcttttag 717

<210> 22
 <211> 723
 <212> PRT
 <213> HIV-2/VCP Clone p16.9 (env)

<400> 22

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
 100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
 115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
 130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
 145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser
 165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
 180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
 195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
 210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
 225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg
405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
 465 470 475 480

Gln Arg His Thr Arg Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu
 485 490 495

Ala Thr Ala Gly Ser Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala
 500 505 510

Gln Ser Arg Thr Ser Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu
 515 520 525

Leu Asp Val Val Lys Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp
 530 535 540

Gly Thr Lys Asn Leu Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu
 545 550 555 560

Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val
 565 570 575

Cys His Thr Ser Val Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp
 580 585 590

Asn Asn Met Thr Trp Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu
 595 600 605

Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys
 610 615 620

Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn
 625 630 635 640

Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr
 645 650 655

Val Val Val Gly Ile Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln
 660 665 670

Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro
 675 680 685

Pro Gly Tyr Ile Gln Gln Ile His Ile His Lys Asp Gln Glu Gln Pro

690

695

700

Ala Arg Glu Glu Thr Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg
 705 710 715 720

Ser Trp Leu

<210> 23
 <211> 485
 <212> PRT
 <213> HIV-2/VCP Clone p16.9 (gp120)
 <400> 23

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
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Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
 100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
 115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
 130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
 145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Ala Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Glu Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Arg Pro Gly Asn Lys Gly Ala
290 295 300

Gly Lys Pro Arg Gln Ala Trp Cys Trp Phe Lys Gly Glu Trp Lys Glu
305 310 315 320

Ala Met Gln Glu Val Lys Glu Thr Leu Ala Lys His Pro Arg Tyr Lys
325 330 335

Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys Phe Lys Ala Pro Gly Arg
340 345 350

Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp Thr Asn Cys Arg Gly Glu
355 360 365

Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu Asn Trp Val Asp Asn Arg
370 375 380

Thr Gly Gln Lys Gln Arg Asn Tyr Ala Pro Cys His Ile Arg Gln Ile
385 390 395 400

Ile Asn Thr Trp His Arg Val Gly Lys Asn Ile Tyr Leu Pro Pro Arg
405 410 415

Glu Gly Glu Leu Thr Cys Asn Ser Thr Val Thr Ser Ile Ile Ala Asn
420 425 430

Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr Phe Ser Ala Glu Val Ala
435 440 445

Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr Lys Leu Val Glu Ile Thr
450 455 460

Pro Ile Gly Phe Ala Pro Thr Ser Val Lys Arg Tyr Ser Ser Ala His
465 470 475 480

Gln Arg His Thr Arg
485

<210> 24
<211> 238
<212> PRT
<213> HIV-2/VCP Clone p16.9 (gp41)

<400> 24

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
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Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys
35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
 100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
 115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
 130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
 145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Val Tyr Val Val Val Gly Ile
 165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
 180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
 195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
 210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu
 225 230 235

<210> 25
 <211> 2142
 <212> DNA
 <213> HIV-2/VCP Clone 8c.3 (env)

<400> 25
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 cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
 aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240
 acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300
 tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc 360
 acagggacca cagacacca aaatatcaca attataaatg acatttcgcc atgcgtacgt 420

gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca	480
ggattagaga gagacaagag aaaacagtat actggaacat ggtactcaaa agatgtgatt	540
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc	600
atcacaaagt catgtgataa gcactattgg gatgctatga ggtttagata ctgtgcacca	660
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ggatttaatg gcactagagc agaaaataga acatatatat attggcatgg taaaaataac	840
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa gggtgccggc	900
tgggtgttgg tcaaaggcga atggaaggaa gccatgcagg aggtgaagga gacccttgcg	960
aaacatccca gatataaagg gaacaggagc cgcacagaga atattaaatt taaagcacca	1020
ggaagaggct cagacccaga agcagcatac atgtggacta actgcagagg ggaatttctc	1080
tactgcaaca tggcttggtt cctcaactgg gtagataaca ggacgggtcg gaaacagcgc	1140
aattatgcac cgtgccatat aaggcaaata attaatactt ggcacagggt agggaaaaac	1200
atatatttgc ctcccaggga aggggagttg gcctgcaact caacagtgac cagcataatt	1260
gccaacattg atacgggaga tcaaacagat attacctta gtgcagagggt ggcagaacta	1320
taccgattgg aattgggaga ttacaaatta gtagaaatca caccaattgg cttcgcacct	1380
acatcagtaa agagatactc ctctgctcac cagagacata caagagggtgt gttcgtgcta	1440
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accgcccagt cccggacttc attggctggg atagtgcagc aacagcaaca gctgttgagc	1560
gtggtcaaga aacaacaaga aatgttgcca ctgaccgtct ggggaactaa aaatctccag	1620
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tgtgcgttta gacaagtctg ccacacttct gtaccatggg taaatgatag cttgacacct	1740
gattggaaca atatgacgtg gcaggaatgg gaacagaaag tccgctactg ggaggcaa	1800
atcagtcaaa gtctagaaca agcacaaatt cagcaagaaa agaatttgta tgagctgcaa	1860
aaattaaata gctgggggtgt ttttaccat tggcttgact tcacctctg ggtcaggtat	1920
attcaatatg gagcatatgt agtagtagga atagtaactt taagaatagt aatatatata	1980
gtacagatgt taagtagact taggaagggc tataggcctg ttttctcctc ccccccggt	2040
tatatccaac agatccatat ccacaaggac caggaacagc cagccagaga agaaacagaa	2100

gaagacgttg gaagcaacgg tggagacaga tcttggcttt ag 2142

<210> 26

<211> 1425

<212> DNA

<213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 26

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cccctgtttt gtgcaaccaa aaatagagat acttggggaa ccatacagtg cttgccagac 180
aatgatgatt atcaggaaat agctctaaat gtaacagagg ctttcgatgc atggaataat 240
acagtaacag aacaagcagt ggaggatgtc tggaatctat ttgagacatc aataaaacca 300
tgtgtcaaat taacaccctt atgtgtagca atgaactgta caaggaacat gaccacatcc 360
acagggacca cagacacca aaatatcaca attataaatg acacttcgcc atgcgtacgt 420
gcagacaact gcacaggatt aaaggaggaa gaaatggtcg actgtcagtt taatatgaca 480
ggattagaga gagacaagag aaaacagtat actggaacat ggtactcaaa agatgtgatt 540
tgtgacaata acacctcaag tcggagcaag tgttacatga accattgcaa tacatcagtc 600
atcacaaagt catgtgataa gcactattgg gatgctatga ggtttagata ctgtgcacca 660
ccgggttttg ccctactaag atgcaatgat actaattatt caggctttgc acctaattgc 720
tctaaagtag tagctgctac atgcaccaga atgatggaaa cgcaatcttc tacatggttt 780
ggatttaatg gcactagagc agaaaataga acatatatat attggcatgg taaaaataac 840
agaactatta tcagcttaaa taacttttat aatctcacta tgcattgtaa ggggtgccgc 900
tggtgttggt tcaaaggcga atggaaggaa gccatgcagg aggtgaagga gacccttgcg 960
aaacatccca gatataaagg gaacaggagc cgcacagaga atattaaatt taaagcacca 1020
ggaagaggct cagaccaga agcagcatac atgtggacta actgcagagg ggaatttctc 1080
tactgcaaca tggcttggtt cctcaactgg gtagataaca ggacgggtcg gaaacagcgc 1140
aattatgcac cgtgccatat aaggcaaata attaatactt ggcacagggt agggaaaaac 1200
atatatttgc ctcccaggga aggggagttg gcctgcaact caacagtgc cagcataatt 1260
gccaacattg atacgggaga tcaaacagat attaccttta gtgcagaggt ggcagaacta 1320
taccgattgg aattgggaga ttacaaatta gtagaaatca caccaattgg cttcgcacct 1380
acatcagtaa agagatactc ctctgctcac cagagacata caaga 1425

<210> 27
 <211> 717
 <212> DNA
 <213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 27
 ggtgtgttcg tgctaggggtt cttggggtttt ctcgcaacgg cagggttctgc aatggg'gcgcg 60
 gcgtcgggtga cgctgaccgc ccagtcccgg acttcattgg ctgggatagt gcagcaacag 120
 caacagctgt tggacgtggt caagaaacaa caagaaatgt tgcgactgac cgtctgggga 180
 actaaaaatc tccagacaag agtcactgct atagagaaat acctaaagga ccaggcgcag 240
 ttaaattcat ggggatgtgc gtttagacaa gtctgccaca cttctgtacc atgggtaaat 300
 gatagcttga cacctgattg gaacaatatg acgtggcagg aatgggaaca gaaagtccgc 360
 tactgggagg caaatatcag tcaaagtcta gaacaagcac aaattcagca agaaaagaat 420
 ttgtatgagc tgcaaaaatt aaatagctgg ggtgttttta ccaattggct tgacttcacc 480
 tcctgggtca ggtatatcca atatggagca tatgtagtag taggaatagt aactttaaga 540
 atagtaatat atatagtaca gatgttaagt agacttagga agggctatag gcctgttttc 600
 tcctcccccc ccggttatat ccaacagatc catatccaca aggaccagga acagccagcc 660
 agagaagaaa cagaagaaga cgttggaagc aacggtggag acagatcttg gcttta’g 717

<210> 28
 <211> 713
 <212> PRT
 <213> HIV-2/VCP Clone ,8c.3 (env)

<400> 28

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser
165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His
195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe
290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala
 305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys
 325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp
 340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu
 355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro
 370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn
 385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val
 405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr
 420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr
 435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys
 450 455 460

Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg Gly Val Phe Val Leu
 465 470 475 480

Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly Ala Ala
 485 490 495

Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser Leu Ala Gly Ile Val
 500 505 510

Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Lys Gln Gln Glu Met
 515 520 525

Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg Val Thr
 530 535 540

Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ser Trp Gly
 545 550 555 560

Cys Ala Phe Arg Gln Val Cys His Thr Ser Val Pro Trp Val Asn Asp
 565 570 575

Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp Gln Glu Trp Glu Gln
 580 585 590

Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln Ser Leu Glu Gln Ala
 595 600 605

Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu Gln Lys Leu Asn Ser
 610 615 620

Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr Ser Trp Val Arg Tyr
 625 630 635 640

Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile Val Thr Leu Arg Ile
 645 650 655

Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu Arg Lys Gly Tyr Arg
 660 665 670

Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln Gln Ile His Ile His
 675 680 685

Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr Glu Glu Asp Val Gly
 690 695 700

Ser Asn Gly Gly Asp Arg Ser Trp Leu
 705 710

<210> 29
 <211> 475
 <212> PRT
 <213> HIV-2/VCP Clone 8c.3 (gp120)

<400> 29

Met Lys Gly Ser Lys Asn Gln Leu Leu Ile Ala Ile Ile Leu Ala Ser
 1 5 10 15

Ala Tyr Leu Thr His Cys Lys Gln Phe Val Thr Val Phe Tyr Gly Ile
 20 25 30

Pro Ala Trp Arg Asn Ala Ser Ile Pro Leu Phe Cys Ala Thr Lys Asn
 35 40 45

Arg Asp Thr Trp Gly Thr Ile Gln Cys Leu Pro Asp Asn Asp Asp Tyr
 50 55 60

Gln Glu Ile Ala Leu Asn Val Thr Glu Ala Phe Asp Ala Trp Asn Asn
 65 70 75 80

Thr Val Thr Glu Gln Ala Val Glu Asp Val Trp Asn Leu Phe Glu Thr
 85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ala Met Asn
 100 105 110

Cys Thr Arg Asn Met Thr Thr Ser Thr Gly Thr Thr Asp Thr Gln Asn
 115 120 125

Ile Thr Ile Ile Asn Asp Thr Ser Pro Cys Val Arg Ala Asp Asn Cys
 130 135 140

Thr Gly Leu Lys Glu Glu Glu Met Val Asp Cys Gln Phe Asn Met Thr
 145 150 155 160

Gly Leu Glu Arg Asp Lys Arg Lys Gln Tyr Thr Gly Thr Trp Tyr Ser
 165 170 175

Lys Asp Val Ile Cys Asp Asn Asn Thr Ser Ser Arg Ser Lys Cys Tyr
 180 185 190

Met Asn His Cys Asn Thr Ser Val Ile Thr Lys Ser Cys Asp Lys His
 195 200 205

Tyr Trp Asp Ala Met Arg Phe Arg Tyr Cys Ala Pro Pro Gly Phe Ala
 210 215 220

Leu Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Ala Pro Asn Cys
 225 230 235 240

Ser Lys Val Val Ala Ala Thr Cys Thr Arg Met Met Glu Thr Gln Ser
245 250 255

Ser Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr
260 265 270

Ile Tyr Trp His Gly Lys Asn Asn Arg Thr Ile Ile Ser Leu Asn Asn
275 280 285

Phe Tyr Asn Leu Thr Met His Cys Lys Gly Ala Gly Trp Cys Trp Phe
290 295 300

Lys Gly Glu Trp Lys Glu Ala Met Gln Glu Val Lys Glu Thr Leu Ala
305 310 315 320

Lys His Pro Arg Tyr Lys Gly Asn Arg Ser Arg Thr Glu Asn Ile Lys
325 330 335

Phe Lys Ala Pro Gly Arg Gly Ser Asp Pro Glu Ala Ala Tyr Met Trp
340 345 350

Thr Asn Cys Arg Gly Glu Phe Leu Tyr Cys Asn Met Ala Trp Phe Leu
355 360 365

Asn Trp Val Asp Asn Arg Thr Gly Arg Lys Gln Arg Asn Tyr Ala Pro
370 375 380

Cys His Ile Arg Gln Ile Ile Asn Thr Trp His Arg Val Gly Lys Asn
385 390 395 400

Ile Tyr Leu Pro Pro Arg Glu Gly Glu Leu Ala Cys Asn Ser Thr Val
405 410 415

Thr Ser Ile Ile Ala Asn Ile Asp Thr Gly Asp Gln Thr Asp Ile Thr
420 425 430

Phe Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp Tyr
435 440 445

Lys Leu Val Glu Ile Thr Pro Ile Gly Phe Ala Pro Thr Ser Val Lys
450 455 460

Arg Tyr Ser Ser Ala His Gln Arg His Thr Arg
 465 470 475

<210> 30
 <211> 238
 <212> PRT
 <213> HIV-2/VCP Clone 8c.3 (gp41)

<400> 30

Gly Val Phe Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser
 1 5 10 15

Ala Met Gly Ala Ala Ser Val Thr Leu Thr Ala Gln Ser Arg Thr Ser
 20 25 30

Leu Ala Gly Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys
 35 40 45

Lys Gln Gln Glu Met Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu
 50 55 60

Gln Thr Arg Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln
 65 70 75 80

Leu Asn Ser Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Ser Val
 85 90 95

Pro Trp Val Asn Asp Ser Leu Thr Pro Asp Trp Asn Asn Met Thr Trp
 100 105 110

Gln Glu Trp Glu Gln Lys Val Arg Tyr Trp Glu Ala Asn Ile Ser Gln
 115 120 125

Ser Leu Glu Gln Ala Gln Ile Gln Gln Glu Lys Asn Leu Tyr Glu Leu
 130 135 140

Gln Lys Leu Asn Ser Trp Gly Val Phe Thr Asn Trp Leu Asp Phe Thr
 145 150 155 160

Ser Trp Val Arg Tyr Ile Gln Tyr Gly Ala Tyr Val Val Val Gly Ile
 165 170 175

Val Thr Leu Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ser Arg Leu
 180 185 190

Arg Lys Gly Tyr Arg Pro Val Phe Ser Ser Pro Pro Gly Tyr Ile Gln
195 200 205

Gln Ile His Ile His Lys Asp Gln Glu Gln Pro Ala Arg Glu Glu Thr
210 215 220

Glu Glu Asp Val Gly Ser Asn Gly Gly Asp Arg Ser Trp Leu
225 230 235